

SEQUENCE LISTING



<110> Amano Enzyme, Inc.

<120> NOVEL ENZYME COMPOSITION AND PRODUCTION METHOD AND USE THEREOF

<130> Q63731

<140> 09/806,413

<141> 2001-03-30

<150> JP 10-294675

<151> 1998-09-30

<160> 16

<170> PatentIn version 3.1

<210> 1

<211> 22

<212> PRT

<213> Aspergillus fumigatus

<400> 1

Ala Ala Ser Ala Ser Ala Tyr Cys Ser Asn Ser Ala Gly Asn Tyr Lys
1 5 10 15

Leu Ser Ser Ile Ala Ala
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<210> 2

<211> 22

<212> PRT

<213> Aspergillus fumigatus

<400> 2

Leu Met Thr Pro Ala Gly Ala Asn Phe Ala Leu Met Arg His Thr Ile
1 5 10 15

Gly Ala Ser Asp Leu Ser
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<210> 3

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic DNA

Part of
Paper 5

DJS
4/25/02

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<222> (14)..(14)
<223> "n" may be a c, g or t

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cggaattcta ytgywsnaay wsngcngg

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 <213> Aspergillus fumigatus

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 gcagctccgg ttcaaggggc cggaaacccc ggctcggaat cgacctggca attgaccggt 120
 gacgacactt cgtccgggtca caaacagacg atagttgggt tcggtgctgc tgtcactgat 180
 gccacgggtca cctcgttcaa cactttgtcc gcctccgtgc tgcaagactt gctcaataaa 240
 ctgatgacac ctgccggggc gaactttgct ttgatgcgac atactattgg ggcttcggat 300
 ctgtccggtg acccagccta cagctacgat gacaatggtg ggaaagcgga tccgtcactg 360
 tcgggattca acctggggga ccgcggaacg gctatggcca agatgttggc aacaatgaag 420
 tctctgcagc ccaacctcaa gatcctcggc tctccctgga gtgcaccagg atggatgaag 480
 ctgaacgggg tccttgatgg caatacgaac aacaacaact tgaacgatgg atacctaacc 540
 agtgggggaa ccggtagtagc ggggtatgcc agtcaattcg cgcagtactt tgtcaagtac 600
 attcaggcct ataagaatct cgggtgctcac gtcgacgcga ttaccatcca gaacgagccg 660
 ctgttcagct cagcgggcta tcccaccatg tatgtctacg attatgagtc ggcacagctg 720
 atccagaact acatcgccc cgctcttgcc agcgcggggc tagatacgga aatctgggct 780
 tatgaccaca acacagatgt cccgtcgtac cccagactg tccttaacca ggccggtcag 840
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 cagttocaca acacaaaccc tggagtgaag caatatatga ccgagtgtg gactccagca 960
 tctggcgcac ggcatcaggc ggcggacttc accatgggtc ccctgcagaa ctgggcctcg 1020
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 ggctgcgcga catgtcaagg cttggtgacc atcaacaacg gaggatacac gctcaacacc 1140
 gcatactaca tgatggcgca attcagcaag ttcattgccg ctggtgcat tgtgctcaat 1200

ggcagtggca gctacacgta ctctggcgga ggcggtatcc agtccgtggc ttccttgaat 1260
cccgatggaa cccgcactgt gggtattgaa aacacttttg gcaatgatgt ctatgtgact 1320
gtcactatga agagcgggca gaagtggagt gggaacgccc ctagccaatc cgtgactacc 1380
tgggttcttc catctgcttg a 1401

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<211> 466
<212> PRT
<213> *Aspergillus fumigatus*

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1 5 10 15

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20 25 30

Glu Ser Thr Trp Gln Leu Thr Val Asp Asp Thr Ser Ser Gly His Lys
35 40 45

Gln Thr Ile Val Gly Phe Gly Ala Ala Val Thr Asp Ala Thr Val Thr
50 55 60

Ser Phe Asn Thr Leu Ser Ala Ser Val Leu Gln Asp Leu Leu Asn Lys
65 70 75 80

Leu Met Thr Pro Ala Gly Ala Asn Phe Ala Leu Met Arg His Thr Ile
85 90 95

Gly Ala Ser Asp Leu Ser Gly Asp Pro Ala Tyr Thr Tyr Asp Asp Asn
100 105 110

Gly Gly Lys Ala Asp Pro Ser Leu Ser Gly Phe Asn Leu Gly Asp Arg
115 120 125

Gly Thr Ala Met Ala Lys Met Leu Ala Thr Met Lys Ser Leu Gln Pro
130 135 140

Asn Leu Lys Ile Leu Gly Ser Pro Trp Ser Ala Pro Gly Trp Met Lys
145 150 155 160

Leu Asn Gly Val Leu Asp Gly Asn Thr Asn Asn Asn Asn Leu Asn Asp
165 170 175

Gly Tyr Leu Thr Ser Gly Gly Thr Gly Ser Thr Gly Tyr Ala Ser Gln
180 185 190

Phe Ala Gln Tyr Phe Val Lys Tyr Ile Gln Ala Tyr Lys Asn Leu Gly
195 200 205

Ala His Val Asp Ala Ile Thr Ile Gln Asn Glu Pro Leu Phe Ser Ser
210 215 220

Ala Gly Tyr Pro Thr Met Tyr Val Tyr Asp Tyr Glu Ser Ala Gln Leu
225 230 235 240

Ile Gln Asn Tyr Ile Gly Pro Ala Leu Ala Ser Ala Gly Leu Asp Thr
245 250 255

Glu Ile Trp Ala Tyr Asp His Asn Thr Asp Val Pro Ser Tyr Pro Gln
260 265 270

Thr Val Leu Asn Gln Ala Gly Gln Tyr Val Lys Ser Val Ala Trp His
275 280 285

Cys Tyr Ala Pro Asn Val Asp Trp Thr Val Leu Ser Gln Phe His Asn
290 295 300

Thr Asn Pro Gly Val Lys Gln Tyr Met Thr Glu Cys Trp Thr Pro Ala
305 310 315 320

Ser Gly Ala Trp His Gln Ala Ala Asp Phe Thr Met Gly Pro Leu Gln
325 330 335

Asn Trp Ala Ser Gly Val Ala Ala Trp Thr Leu Gly Thr Asn Ala Gln
340 345 350

Asp Gly Pro His Leu Ser Thr Gly Gly Cys Ala Thr Cys Gln Gly Leu
355 360 365

Val Thr Ile Asn Asn Gly Gly Tyr Thr Leu Asn Thr Ala Tyr Tyr Met
370 375 380

Met Ala Gln Phe Ser Lys Phe Met Pro Pro Gly Ala Ile Val Leu Asn
 385 390 395 400

Gly Ser Gly Ser Tyr Thr Tyr Ser Gly Gly Gly Gly Ile Gln Ser Val
 405 410 415

Ala Ser Leu Asn Pro Asp Gly Thr Arg Thr Val Val Ile Glu Asn Thr
 420 425 430

Phe Gly Asn Asp Val Tyr Val Thr Val Thr Met Lys Ser Gly Gln Lys
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Trp Ser Gly Asn Ala Pro Ser Gln Ser Val Thr Thr Trp Val Leu Pro
 450 455 460

Ser Ala
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<210> 9
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 <212> DNA
 <213> Aspergillus fumigatus

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 Met

cgt ata tct gtc ggt gct ctg ctt ggc ttg aca gcc ctg agt cat gcc 104
 Arg Ile Ser Val Gly Ala Leu Leu Gly Leu Thr Ala Leu Ser His Ala
 -20 -15 -10

aca aca gag aaa cga gcc gcc tct gct tcg gct tac tgt tcc aac tcg 152
 Thr Thr Glu Lys Arg Ala Ala Ser Ala Ser Ala Tyr Cys Ser Asn Ser
 -5 -1 1 5 10

gcc ggc aac tac aag ctg tcc tcc atc gca gct ccg gtt caa ggg gcc	200
Ala Gly Asn Tyr Lys Leu Ser Ser Ile Ala Ala Pro Val Gln Gly Ala	
15 20 25	
gga aac ccc ggc tcg gaa tcg acc tgg caa ttg acc gtt gac gac act	248
Gly Asn Pro Gly Ser Glu Ser Thr Trp Gln Leu Thr Val Asp Asp Thr	
30 35 40	
tcg tcc ggt cac aaa cag acg ata gtt ggg ttc ggt gct gct gtc act	296
Ser Ser Gly His Lys Gln Thr Ile Val Gly Phe Gly Ala Ala Val Thr	
45 50 55	
gat gcc acg gtc acc tcg ttc aac act ttg tcc gcc tcc gtg ctg caa	344
Asp Ala Thr Val Thr Ser Phe Asn Thr Leu Ser Ala Ser Val Leu Gln	
60 65 70 75	
gac ttg ctc aat aaa ctg atg aca cct gcc ggg gcg aac ttt gct ttg	392
Asp Leu Leu Asn Lys Leu Met Thr Pro Ala Gly Ala Asn Phe Ala Leu	
80 85 90	
atg cga cat act att ggg gct tcg gat ctg tcc ggt gac cca gcc tac	440
Met Arg His Thr Ile Gly Ala Ser Asp Leu Ser Gly Asp Pro Ala Tyr	
95 100 105	
acg tac gat gac aat ggt ggg aaa gcg gat ccg tca ctg tcg gga ttc	488
Thr Tyr Asp Asp Asn Gly Gly Lys Ala Asp Pro Ser Leu Ser Gly Phe	
110 115 120	
aac ctg ggg gac cgc gga acg gct atg gcc aag atg ttg gca aca atg	536
Asn Leu Gly Asp Arg Gly Thr Ala Met Ala Lys Met Leu Ala Thr Met	
125 130 135	
aag tct ctg cag ccc aac ctc aag atc ctc ggc tct ccc tgg agt gca	584
Lys Ser Leu Gln Pro Asn Leu Lys Ile Leu Gly Ser Pro Trp Ser Ala	
140 145 150 155	
cca gga tgg atg aag ctg aac ggg gtc ctt gat ggc aat acg aac aac	632
Pro Gly Trp Met Lys Leu Asn Gly Val Leu Asp Gly Asn Thr Asn Asn	
160 165 170	
aac aac ttg aac gat gga tac cta acc agt ggg gga acc ggt agt acg	680
Asn Asn Leu Asn Asp Gly Tyr Leu Thr Ser Gly Gly Thr Gly Ser Thr	
175 180 185	
ggg tat gcc agt caa ttc gcg cag tac ttt gtc aag tac att cag gcc	728
Gly Tyr Ala Ser Gln Phe Ala Gln Tyr Phe Val Lys Tyr Ile Gln Ala	
190 195 200	
tat aag aat ctc ggt gct cac gtc gac gcg att acc atc cag aac gag	776
Tyr Lys Asn Leu Gly Ala His Val Asp Ala Ile Thr Ile Gln Asn Glu	
205 210 215	
ccg ctg ttc agc tca gcg ggc tat ccc acc atg tat gtc tac gat tat	824
Pro Leu Phe Ser Ser Ala Gly Tyr Pro Thr Met Tyr Val Tyr Asp Tyr	

220	225	230	235	
gag tcg gca cag ctg atc cag aac tac atc ggc ccc gct ctt gcc agc				872
Glu Ser Ala Gln Leu Ile Gln Asn Tyr Ile Gly Pro Ala Leu Ala Ser				
	240	245	250	
gcg ggg cta gat acg gaa atc tgg gct tat gac cac aac aca gat gtc				920
Ala Gly Leu Asp Thr Glu Ile Trp Ala Tyr Asp His Asn Thr Asp Val				
	255	260	265	
ccg tcg tac ccc cag act gtc ctt aac cag gcc ggt cag tac gtc aag				968
Pro Ser Tyr Pro Gln Thr Val Leu Asn Gln Ala Gly Gln Tyr Val Lys				
	270	275	280	
tcg gtg gcc tgg cac tgc tac gct ccc aac gtc gac tgg acc gtg ctc				1016
Ser Val Ala Trp His Cys Tyr Ala Pro Asn Val Asp Trp Thr Val Leu				
	285	290	295	
agc cag ttc cac aac aca aac cct gga gtg aag caa tat atg acc gag				1064
Ser Gln Phe His Asn Thr Asn Pro Gly Val Lys Gln Tyr Met Thr Glu				
300	305	310	315	
tgc tgg act cca gca tct ggc gca tgg cat cag gcg gcg gac ttc acc				1112
Cys Trp Thr Pro Ala Ser Gly Ala Trp His Gln Ala Ala Asp Phe Thr				
	320	325	330	
atg ggt ccc ctg cag aac tgg gcc tcg gga gtg gca gca tgg act ctg				1160
Met Gly Pro Leu Gln Asn Trp Ala Ser Gly Val Ala Ala Trp Thr Leu				
	335	340	345	
gga acc aac gct cag gat ggt ccg cat ctg tcc act ggc ggc tgc gcg				1208
Gly Thr Asn Ala Gln Asp Gly Pro His Leu Ser Thr Gly Gly Cys Ala				
	350	355	360	
aca tgt caa ggc ttg gtg acc atc aac aac gga gga tac acg ctc aac				1256
Thr Cys Gln Gly Leu Val Thr Ile Asn Asn Gly Gly Tyr Thr Leu Asn				
	365	370	375	
acc gca tac tac atg atg gcg caa ttc agc aag ttc atg ccg cct ggt				1304
Thr Ala Tyr Tyr Met Met Ala Gln Phe Ser Lys Phe Met Pro Pro Gly				
380	385	390	395	
gcg att gtg ctc aat ggc agt ggc agc tac acg tac tct ggc gga ggc				1352
Ala Ile Val Leu Asn Gly Ser Gly Ser Tyr Thr Tyr Ser Gly Gly Gly				
	400	405	410	
ggt atc cag tcc gtg gct tcc ttg aat ccc gat gga acc cgc act gtg				1400
Gly Ile Gln Ser Val Ala Ser Leu Asn Pro Asp Gly Thr Arg Thr Val				
	415	420	425	
gtt att gaa aac act ttt ggc aat gat gtc tat gtg act gtc act atg				1448
Val Ile Glu Asn Thr Phe Gly Asn Asp Val Tyr Val Thr Val Thr Met				
	430	435	440	
aag agc ggg cag aag tgg agt ggg aac gcc cct agc caa tcc gtg act				1496

Lys Ser Gly Gln Lys Trp Ser Gly Asn Ala Pro Ser Gln Ser Val Thr
 445 450 455

acc tgg gtt ctt cca tct gct tgaaaagagt gtagtttcag atgggttagat 1547
 Thr Trp Val Leu Pro Ser Ala
 460 465

atgtattgaa gagtagcgct tggagacatc aatagccttt ttctaattac atgtcgtgca 1607

gcttccaaaa aaaaaaaaaa aaaaaaaaaa aaaaactcga 1647

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 <212> PRT
 <213> Aspergillus fumigatus

<400> 10

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 -5 -1 1 5 10

Ser Ala Gly Asn Tyr Lys Leu Ser Ser Ile Ala Ala Pro Val Gln Gly
 15 20 25

Ala Gly Asn Pro Gly Ser Glu Ser Thr Trp Gln Leu Thr Val Asp Asp
 30 35 40

Thr Ser Ser Gly His Lys Gln Thr Ile Val Gly Phe Gly Ala Ala Val
 45 50 55

Thr Asp Ala Thr Val Thr Ser Phe Asn Thr Leu Ser Ala Ser Val Leu
 60 65 70

Gln Asp Leu Leu Asn Lys Leu Met Thr Pro Ala Gly Ala Asn Phe Ala
 75 80 85 90

Leu Met Arg His Thr Ile Gly Ala Ser Asp Leu Ser Gly Asp Pro Ala
 95 100 105

Tyr Thr Tyr Asp Asp Asn Gly Gly Lys Ala Asp Pro Ser Leu Ser Gly
 110 115 120

Phe Asn Leu Gly Asp Arg Gly Thr Ala Met Ala Lys Met Leu Ala Thr
125 130 135

Met Lys Ser Leu Gln Pro Asn Leu Lys Ile Leu Gly Ser Pro Trp Ser
140 145 150

Ala Pro Gly Trp Met Lys Leu Asn Gly Val Leu Asp Gly Asn Thr Asn
155 160 165 170

Asn Asn Asn Leu Asn Asp Gly Tyr Leu Thr Ser Gly Gly Thr Gly Ser
175 180 185

Thr Gly Tyr Ala Ser Gln Phe Ala Gln Tyr Phe Val Lys Tyr Ile Gln
190 195 200

Ala Tyr Lys Asn Leu Gly Ala His Val Asp Ala Ile Thr Ile Gln Asn
205 210 215

Glu Pro Leu Phe Ser Ser Ala Gly Tyr Pro Thr Met Tyr Val Tyr Asp
220 225 230

Tyr Glu Ser Ala Gln Leu Ile Gln Asn Tyr Ile Gly Pro Ala Leu Ala
235 240 245 250

Ser Ala Gly Leu Asp Thr Glu Ile Trp Ala Tyr Asp His Asn Thr Asp
255 260 265

Val Pro Ser Tyr Pro Gln Thr Val Leu Asn Gln Ala Gly Gln Tyr Val
270 275 280

Lys Ser Val Ala Trp His Cys Tyr Ala Pro Asn Val Asp Trp Thr Val
285 290 295

Leu Ser Gln Phe His Asn Thr Asn Pro Gly Val Lys Gln Tyr Met Thr
300 305 310

Glu Cys Trp Thr Pro Ala Ser Gly Ala Trp His Gln Ala Ala Asp Phe
315 320 325 330

Thr Met Gly Pro Leu Gln Asn Trp Ala Ser Gly Val Ala Ala Trp Thr
335 340 345

Leu Gly Thr Asn Ala Gln Asp Gly Pro His Leu Ser Thr Gly Gly Cys
350 355 360

Ala Thr Cys Gln Gly Leu Val Thr Ile Asn Asn Gly Gly Tyr Thr Leu
365 370 375

Asn Thr Ala Tyr Tyr Met Met Ala Gln Phe Ser Lys Phe Met Pro Pro
380 385 390

Gly Ala Ile Val Leu Asn Gly Ser Gly Ser Tyr Thr Tyr Ser Gly Gly
395 400 405 410

Gly Gly Ile Gln Ser Val Ala Ser Leu Asn Pro Asp Gly Thr Arg Thr
415 420 425

Val Val Ile Glu Asn Thr Phe Gly Asn Asp Val Tyr Val Thr Val Thr
430 435 440

Met Lys Ser Gly Gln Lys Trp Ser Gly Asn Ala Pro Ser Gln Ser Val
445 450 455

Thr Thr Trp Val Leu Pro Ser Ala
460 465

<210> 11
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<213> Artificial Sequence

<220>
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<210> 14
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